

FIG 1

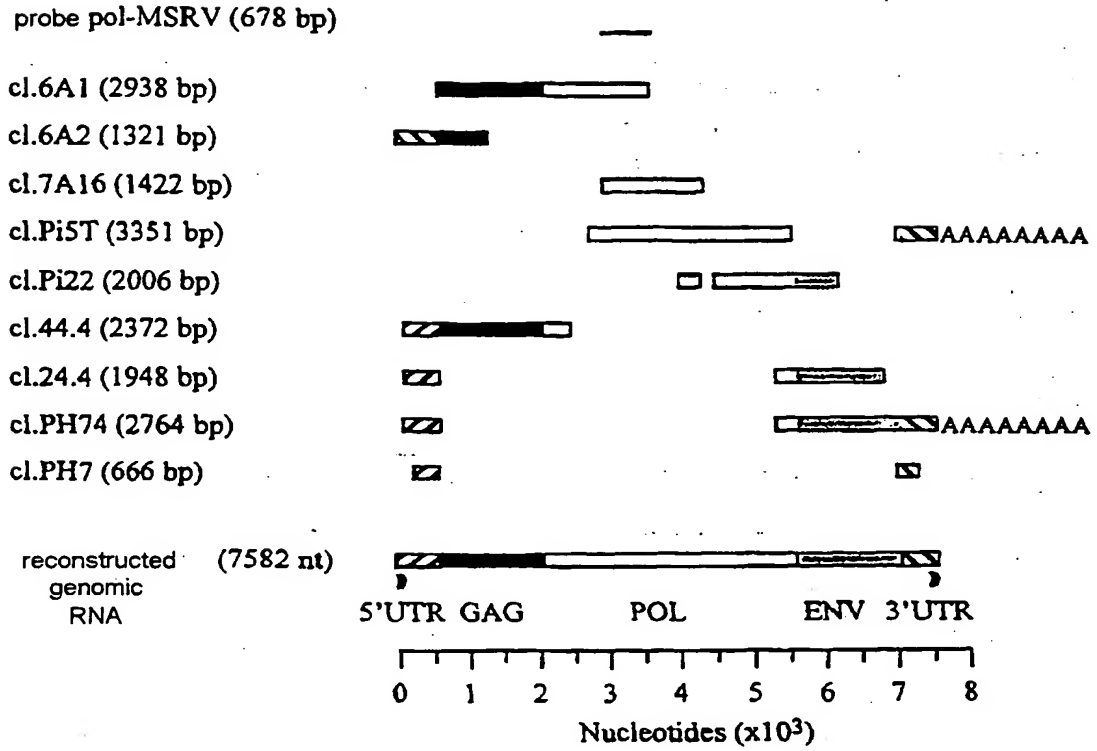
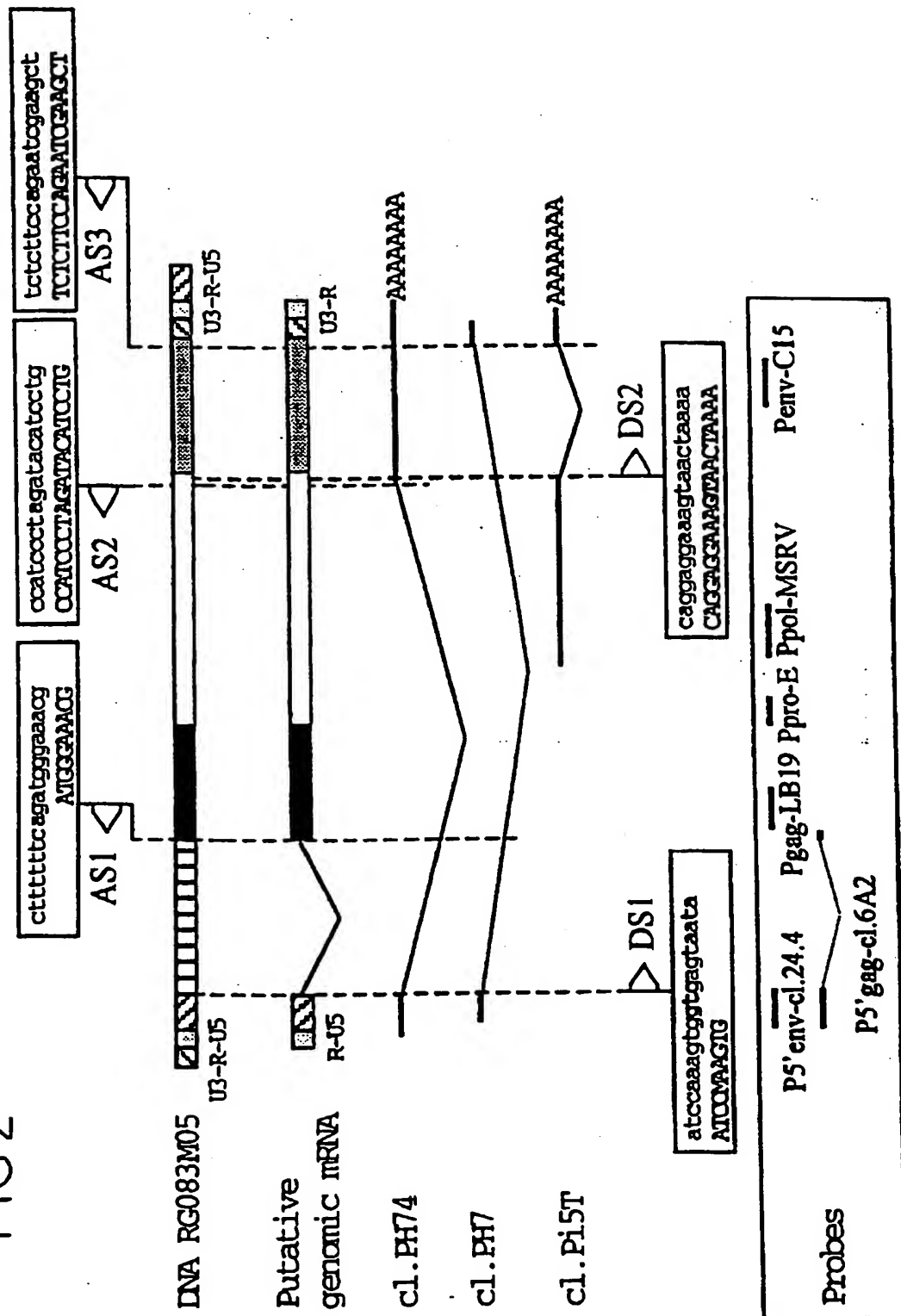


FIG 2



# FIG 3

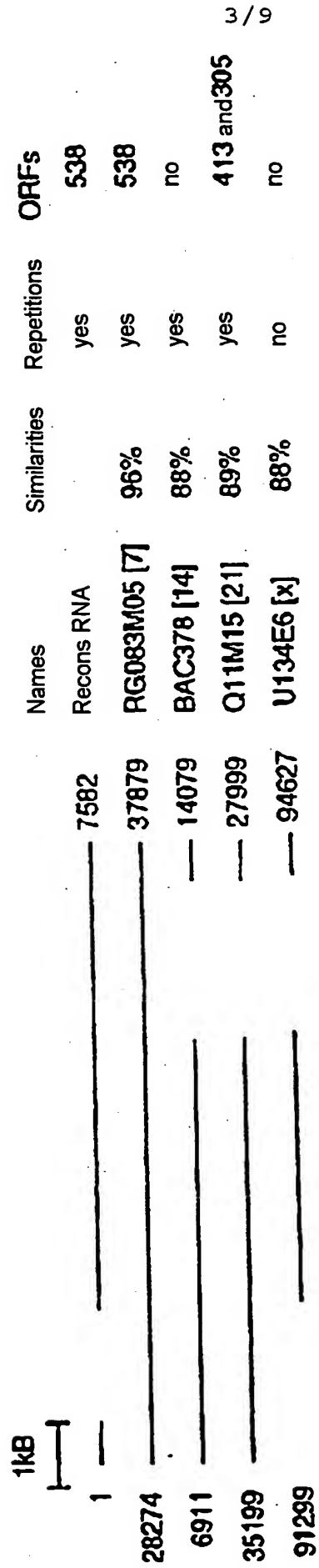


FIG 4A

LTR

0.02

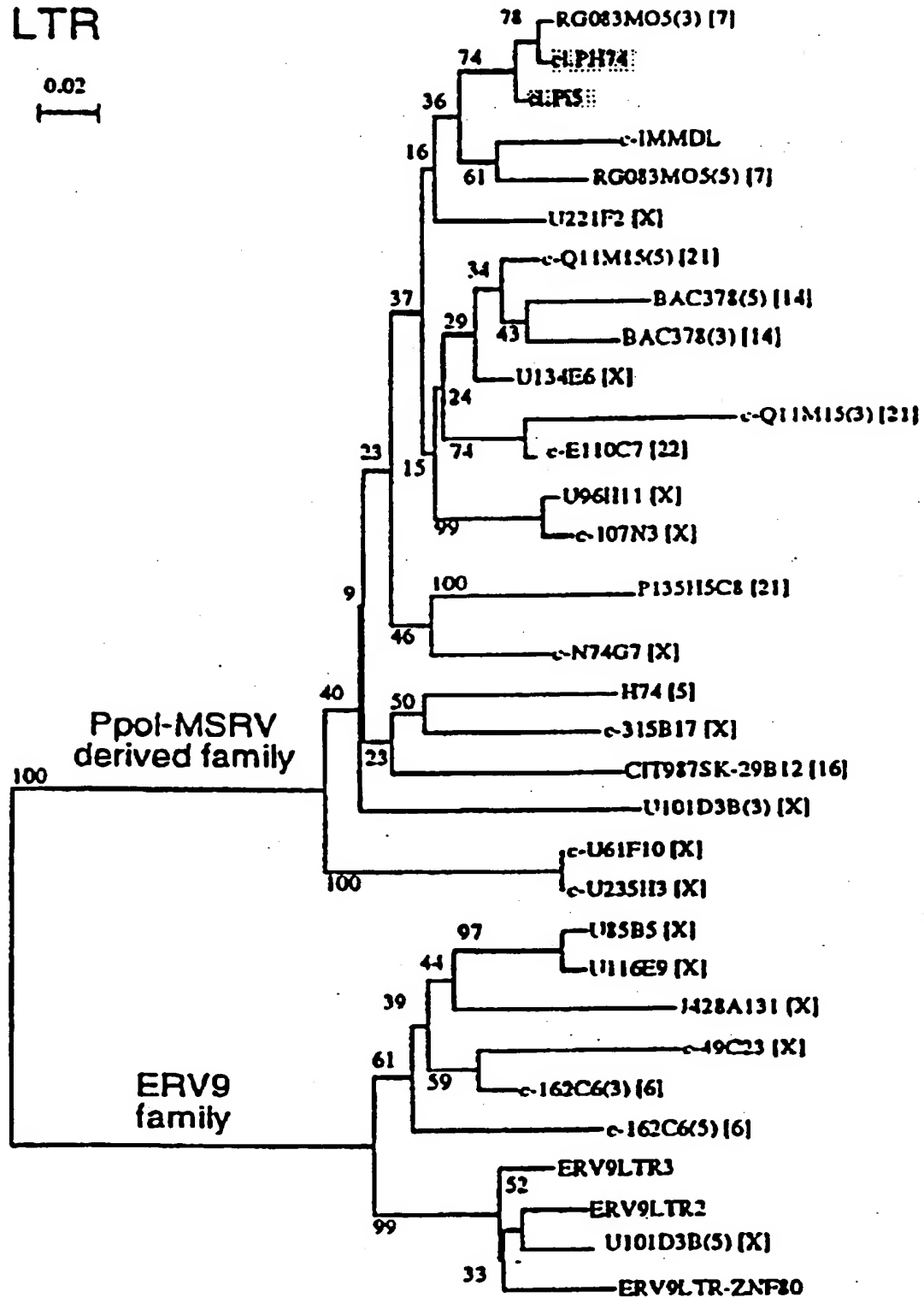


FIG 4 B

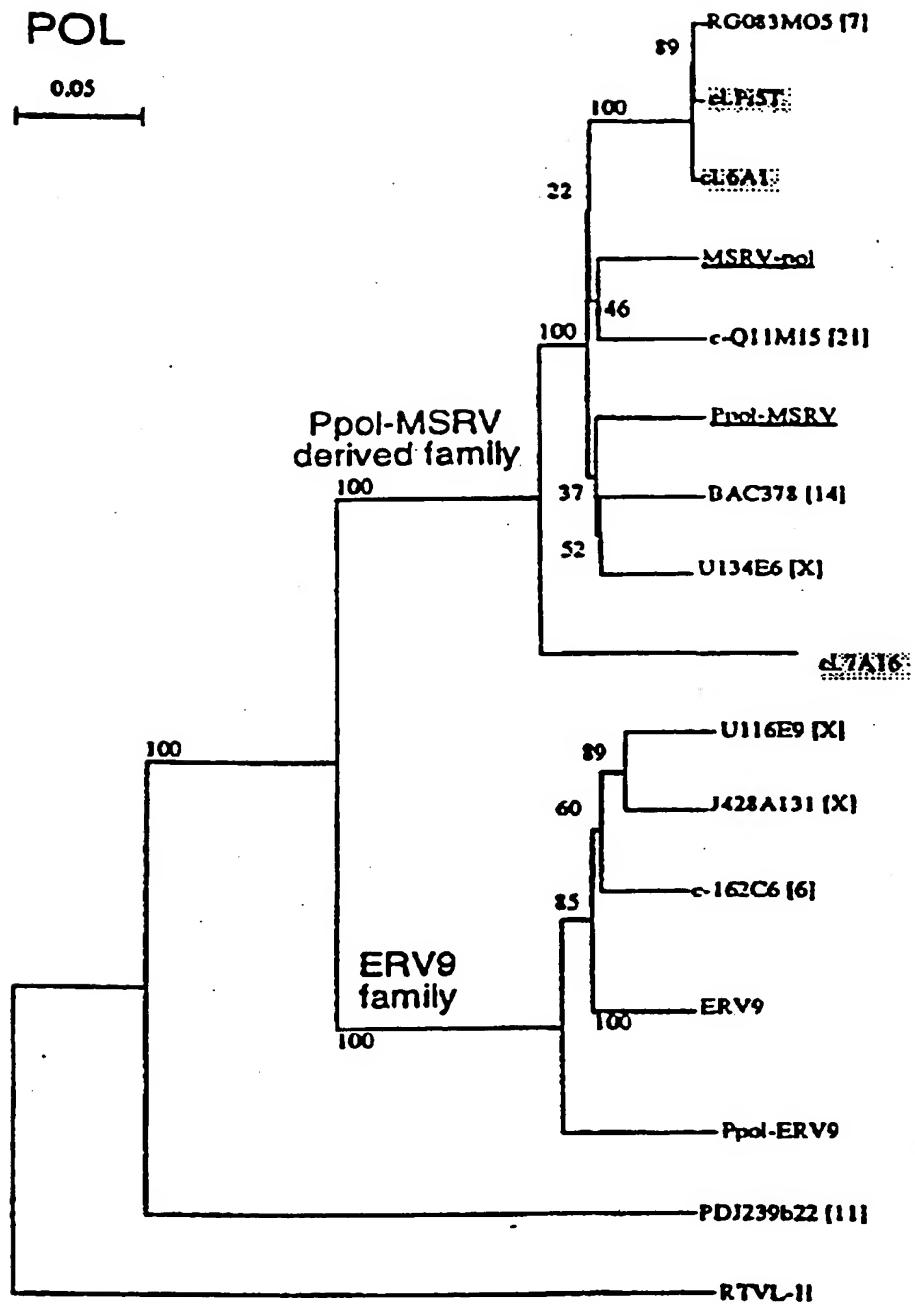
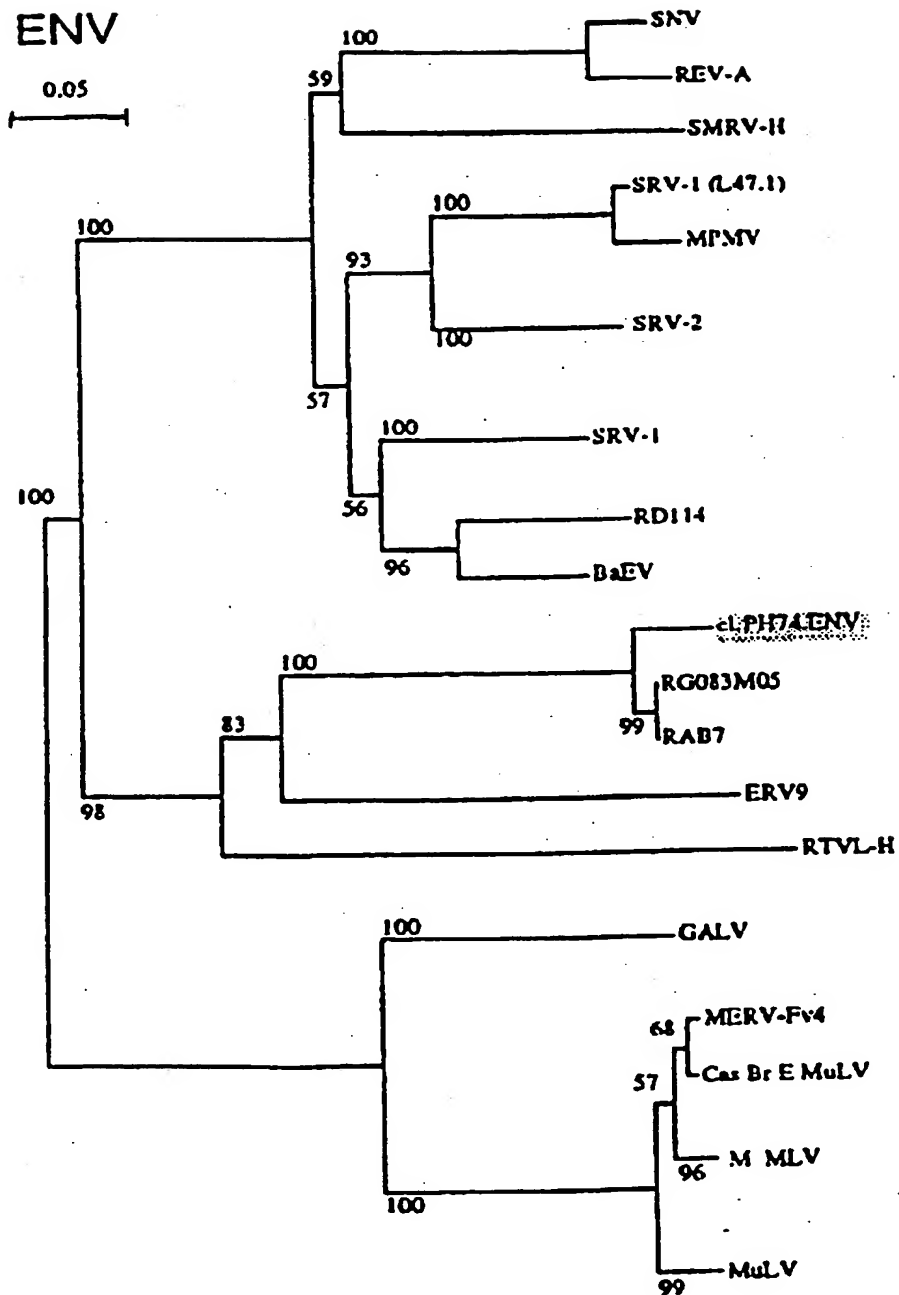


FIG 4C



[illegible]

# FIG 5B

5-RG-28000-28872	CCGCA GACCTGGGCTGAC TCCATCCCTCTGATCCCTGCA GGGGTGCTGGCTGTGTCTCTGATCCAGCGAGGGGCTTAAAGGCTTGGCCATTGTGTTCTGTC	585
3-RG-37500-38314	CCGCA GACCTGGGCTGAC TCCATCCCTCTGATCCCTGCA GGGGTGCTGGCTGTGTCTCTGATCCAGCGAGGGGCTTAAAGGCTTGGCCATTGTGTTCTGTC	572
5-6A2.1-600	CCGCA GACCTGGGCTGAC TCCATCCCTCTGATCCCTGCA GGGGTGCTGGCTGTGTCTCTGATCCAGCGAGGGGCTTAAAGGCTTGGCCATTGTGTTCTGTC	312
5-PH74.1-530	CCGCA GACCTGGGCTGAC TCCATCCCTCTGATCCCTGCA GGGGTGCTGGCTGTGTCTCTGATCCAGCGAGGGGCTTAAAGGCTTGGCCATTGTGTTCTGTC	241
5-24.4.1-486	CCGCA GACCTGGGCTGAC TCCATCCCTCTGATCCCTGCA GGGGTGCTGGCTGTGTCTCTGATCCAGCGAGGGGCTTAAAGGCTTGGCCATTGTGTTCTGTC	198
Consensus	CCGCA GACCTGGGCTGAC TCCATCCCTCTGATCCCTGCA GGGGTGCTGGCTGTGTCTCTGATCCAGCGAGGGGCTTAAAGGCTTGGCCATTGTGTTCTGTC	520
5-RG-28000-28872	ACGGCTAAGTGGCTGGGTTTGTAAATTGAGCTGAACACTAGTCTAGGTTCCATGGGTTCTCTCTGTGACCCACGGCTTCTAATAGACTATATACACTTACACATGGCCCAAGATT	705
3-RG-37500-38314	ATGGCTAAGTGGCTGGGTTTGTAAATTGAGCTGAACACTAGTCTAGGTTCCATGGGTTCTCTCTGTGACCCACGGCTTCTAATAGACTATATACACTTACACATGGCCCAAGATT	692
5-6A2.1-600	ACGGCTAAGTGGCTGGGTTTGTAAATTGAGCTGAACACTAGTCTAGGTTCCATGGGTTCTCTCTGTGACCCACGGCTTCTAATAGACTATATACACTTACACATGGCCCAAGATT	432
5-PH74.1-530	ACGGCTAAGTGGCTGGGTTTGTAAATTGAGCTGAACACTAGTCTAGGTTCCATGGGTTCTCTCTGTGACCCACGGCTTCTAATAGACTATATACACTTACACATGGCCCAAGATT	361
5-24.4.1-486	ACGGCTAAGTGGCTGGGTTTGTAAATTGAGCTGAACACTAGTCTAGGTTCCATGGGTTCTCTCTGTGACCCACGGCTTCTAATAGACTATATACACTTACACATGGCCCAAGATT	318
Consensus	ACGGCTAAGTGGCTGGGTTTGTAAATTGAGCTGAACACTAGTCTAGGTTCCATGGGTTCTCTCTGTGACCCACGGCTTCTAATAGACTATATACACTTACACATGGCCCAAGATT	640
5-RG-28000-28872	CCATTCTTGGGATTCCTTTAGGSCAAGGACTTCCASGTCGAGGATACGAGGCTTGGCCACCATCTTGGAGGGGCTTGGCTTACCCACCATCTTGGGAGCTCTTG	824
3-RG-37500-38314	CCATTCTTGGGATTCCTTTAGGSCAAGGACTTCCASGTCGAGGATACGAGGCTTGGCCACCATCTTGGAGGGGCTTGGCTTACCCACCATCTTGGGAGCTCTTG	766
5-6A2.1-600	CCATTCTTGGGATTCCTTTAGGSCAAGGACTTCCASGTCGAGGATACGAGGCTTGGCCACCATCTTGGAGGGGCTTGGCTTACCCACCATCTTGGGAGCTCTTG	551
5-PH74.1-530	CCATTCTTGGGATTCCTTTAGGSCAAGGACTTCCASGTCGAGGATACGAGGCTTGGCCACCATCTTGGAGGGGCTTGGCTTACCCACCATCTTGGGAGCTCTTG	481
5-24.4.1-486	CCATTCTTGGGATTCCTTTAGGSCAAGGACTTCCASGTCGAGGATACGAGGCTTGGCCACCATCTTGGAGGGGCTTGGCTTACCCACCATCTTGGGAGCTCTTG	437
Consensus	CCATTCTTGGGATTCCTTTAGGSCAAGGACTTCCASGTCGAGGATACGAGGCTTGGCCACCATCTTGGAGGGGCTTGGCTTACCCACCATCTTGGGAGCTCTTG	760
5-RG-28000-28872	TGAGCAAGGACCCCTCCGTTACATTTTGGCAACGACGACGACATCCA	873
3-RG-37500-38314	TGAGCAAGGACCCCTCCGTTACATTTTGGCAACGACGACGACATCCA	815
5-6A2.1-600	TGAGCAAGGACCCCTCCGTTACATTTTGGCAACGACGACGACATCCA	600
5-PH74.1-530	TGAGCAAGGACCCCTCCGTTACATTTTGGCAACGACGACGACATCCA	530
5-24.4.1-486	TGAGCAAGGACCCCTCCGTTACATTTTGGCAACGACGACGACATCCA	486
Consensus	TGAGCAAGGACCCCTCCGTTACATTTTGGCAACGACGACGACATCCA	783



# ORF1: ENV (538 AA) FIG 6

```

<--- L --->--- SU
MGLPYHIFLCVLSPCFTLTAPPPCRMTSSSPHPEFLWRMQRPGNIDAPSYRSLSKGTP 60
A FT V S YQ C

TFTAHTHMPRNCYHSATLCMHANTHYWTGKMINPSCPGLGVTVCWTYFTQTGMSDGGGV 120

QDQAREKHVKEVISOLTG VHGTS SPYKGLDLSKLHETLRTHTRLVSLFNTTLTGLHEVSA 180
R

QNPTNCWICLPLNFRPYVSI PVPEQWNNFSTEINTTSVLVGPLVSNVEITHTSNLTCVKF 240
L

SNTTYTTNSQCIRWVTPPTQIVCLPSGIFVCGTSAYRCLNGSSESMCFLSFLVPPMAIY 300
T

----->--- TM
TEQDLYSYVISKPRNKRVPILPFVIGAGVLGALGTGIGGITTSTQFYKLSQELNGDMER 360

VADSLVTLODQLNSLA AVLQNRALDLLTAERGGTCLFLGEECCYYVNQSGIVTEKVEE 420
R S K

IPDRIQRIAEELRNTGPWGLLSRWMPWILPFLGPLAAIILLLLFGPCIFDLLVNFVSSRI 480
R R Q N

EAVKLQMEPKMQSKTKIYRRPLDRPASPRSDVNDIKGTPPEEISAAQPLLRPNSAGSS 538

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## ORF2 (52AA)

MEPKMQSKTKIYRRPLDRPVSPRSDVNDIKGTPPEEISAAQPLLRPNSAGSS-

Alignment ORF2 and Rex PLLV-L

```

ORF2          KIY-RRPLDRPASPRSDVNDIKGTPPEEISAAQPLLRP
++Y          LD P SP ++          P S QPLLRP
Rex PTLV-L (B53482) RLYNTLSLDSPPSPKELPA-----PSRFSPQPLLRP

```

## ORF3 (48AA)

MLMTSKAPLLRKSQ LHNLYYAPIQQEAVRAVVGQPPQHLGFPVEMGD

Alignment ORF3 and Tat SIV-AGM

```

ORF3          MTSKAPLLRKSQ LHNLYYAPIQQEAVRAVVGQPPQ
+T AP R+ ++ +L AP+Q +++ G+ Q
Tat SIV-AGM(p05913) VTYHAPRTRRKKIRSLNLAPLQHQSISTKWGRDGO

```